AMENDMENTS

IN THE SPECIFICATION

Please replace the paragraph beginning at page 4, line 21 with the following rewritten paragraph:

--Figures 1A, 1B, 1C and 1D depict several configurations for attachment of the target sequences to the arrays of the invention. Bead arrays are depicted, although as outlined herein, any number of additional arrays may be used. Figure 1A depicts a substrate **5** with a capture probe **20** attached via an optional attachment linker **15** to an associated microsphere **10**. Target sequence **25** comprises target positions **30, 31, 32,** and **33** with a sequencing primer **40** hybridized adjacently to these positions. There may be any number of sets of target positions ($n \geq 1$). Figure 1B depicts the use of the capture probe **20** as the sequencing primer. Figure 1C depicts the use of a capture extender probe (sometimes referred to herein as an "adapter probe") **100** that has a first domain that hybridizes to the capture probe **20** and a second portion that hybridizes to the target sequence **25**. Figure 1D shows the direct attachment of the target sequence **25** to the bead **10**.--

IN THE CLAIMS

Please amend claims 1-6, 10, 12 and 18 as follows:

1. (Amended) A method of sequencing first and second target nucleic acids each comprising a first domain and an adjacent second domain, said second domain comprising a plurality of target positions, said method comprising:
a) providing first and second hybridization complexes comprising first and second target sequences, respectively and first and second sequencing primers, respectively, that hybridize to the first domain of said first and second target